

SEQUENCE LISTING

<110> Sibley, David R.

Monsma, Frederick J.

Hamblin, Mark

<220>

<223> primer

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- 2 -

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	ctcaa															471
gic	cca		agu											Ser 10		
	cca Pro															519
tgg Trp	gtg Val	gct Ala 30	gcc Ala	gcg Ala	ctg Leu	tgc Cys	gtg Val 35	gtc Val	atc Ile	gtg Val	ctg Leu	aca Thr 40	gca Ala	gcc Ala	gcc Ala	567
	tcg Ser 45															615
	tct Ser															663
	ttg Leu															711
tgg Trp	gtg Val	tta Leu	gct Ala 95	cga Arg	ggc Gly	ctc Leu	tgt Cys	ctg Leu 100	ctt Leu	tgg Trp	act Thr	gcc Ala	ttc Phe 105	gac Asp	gtg Val	759
	tgc Cys															807
	tac Tyr 125															855
	ccg Pro															903
	gcc Ala															951
	cga Arg															999
	gtc Val															104

•.

Ile Cys Phe Thr Tyr Cys Arg Ile Leu Leu Ala Ala Arg Lys Gln Ala 210 qtq caa qtq qcc tcq ctc acc acq qqc acq gct gqc cag gcc ttg gaa Val Gln Val Ala Ser Leu Thr Thr Gly Thr Ala Gly Gln Ala Leu Glu 225 230 ace ttg cag gtg ccc agg aca cca cgc cca ggg atg gag tcc gct gac 1191 Thr Leu Gln Val Pro Arg Thr Pro Arg Pro Gly Met Glu Ser Ala Asp 245 240 agt agg cgt ctg gcc acc aag cat agc agg aag gcc ttg aag gcc agc 1239 Ser Arg Arg Leu Ala Thr Lys His Ser Arg Lys Ala Leu Lys Ala Ser 255 260 ctg acc ctg ggc atc ctg ctg gga atg ttc ttt gtc acc tgg ctg ccc 1287 Leu Thr Leu Gly Ile Leu Leu Gly Met Phe Phe Val Thr Trp Leu Pro 270 275 1335 ttc ttt gtg gcc aac ata gct cag gcc gtg tgt gac tgc atc tcc cca Phe Phe Val Ala Asn Ile Ala Gln Ala Val Cys Asp Cys Ile Ser Pro 285 290 qqc ctc ttc qat qtc ctc aca tqq ctg ggg tac tgt aat agc acc atg 1383 Gly Leu Phe Asp Val Leu Thr Trp Leu Gly Tyr Cys Asn Ser Thr Met 310 315 300 305 aac cct atc atc tac ccg ctc ttt atg cgg gac ttc aag agg gcc ctg Asn Pro Ile Ile Tyr Pro Leu Phe Met Arg Asp Phe Lys Arg Ala Leu 320 ggc agg ttc ctg cat gcg tcc act gtc ccc cgg agc acc ggc cag ccc Gly Arg Phe Leu His Ala Ser Thr Val Pro Arg Ser Thr Gly Gln Pro 335 tgc ctc ccc ctc cat gtg gac ctc tca cag cgg tgc cag acc agg cct Cys Leu Pro Leu His Val Asp Leu Ser Gln Arg Cys Gln Thr Arg Pro caq ctq caq qtq ctc gct ctg cct ctg ccg cca aac tca gat tca 1575 Gln Leu Gln Gln Val Leu Ala Leu Pro Leu Pro Pro Asn Ser Asp Ser 365 370 375 1623 qae tee get tea ggg gge ace teg gge etg cag etc aca gee cag ett Asp Ser Ala Ser Gly Gly Thr Ser Gly Leu Gln Leu Thr Ala Gln Leu 395 380 385 390 Leu Leu Pro Gly Glu Ala Thr Arg Asp Pro Pro Pro Pro Thr Arg Ala 410 400 405 acc act gtg gtc aac ttc ttt gtc aca gac tct gtg gag cct gag ata 1719 Thr Thr Val Val Asn Phe Phe Val Thr Asp Ser Val Glu Pro Glu Ile 415 420

cgg ccg cat cca ctc agt tcc ccc gtg aac tgaccaggtc aagagctggc 1769
Arg Pro His Pro Leu Ser Ser Pro Val Asn
430 435

cattggagge cacatteceg gageteteag eccaetetee etgagaetag gaggtggtag 1829 gteteetgag agtgtgetga attgaggtat eteagetage ceatettetg etgeagetee 1889 ttgaetgagg ggtagteaga eacat

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<213> Rat

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330 335 325 Ala Ser Thr Val Pro Arg Ser Thr Gly Gln Pro Cys Leu Pro Leu His 345 Val Asp Leu Ser Gln Arg Cys Gln Thr Arg Pro Gln Leu Gln Gln Val 360 Leu Ala Leu Pro Leu Pro Pro Asn Ser Asp Ser Asp Ser Ala Ser Gly 375 Gly Thr Ser Gly Leu Gln Leu Thr Ala Gln Leu Leu Pro Gly Glu 390 395 400 Ala Thr Arg Asp Pro Pro Pro Pro Thr Arg Ala Thr Thr Val Val Asn 410 Phe Phe Val Thr Asp Ser Val Glu Pro Glu Ile Arg Pro His Pro Leu 425 Ser Ser Pro Val Asn 435 <210> 9 <211> 2108 <212> DNA <213> Rat <220> <221> CDS <222> (439)...(1311) <221> intron <222> (1312)...(1505) <221> CDS <222> (1506)...(1943) <400> 9 ccaaccccca cgcgcgacac gtggtgatct aacgtactca cacgcccacc cttctcgaag 60 agactgcccc ggccggaagg cgggagttcg gctcctgctc ccacatcccc agctgtgccc 120 ctagccagga accccaccc catcttatgg catcccggt ggccctattc catcccaggg 180 ctctcatcca gccccaagct aactttcatt gactcgtcac atcagtaccc ctccccaaac 240 ttcttacccq aqtactccaq qtqqccctqc gtaggaggca cccctacaac tcctcccgat 300 ctcttgaaat cgctgctcga tgacctaaga accccgtttt gccaatacta ctctaaggtg 360 caqcttcctt tetectectt tqccttcace etqtacetqe aqtcaccata tecegtettg 420 gtcctcaacc cagtcccc atg gtt cca gag cca ggc cct gtc aac agt agc Met Val Pro Glu Pro Gly Pro Val Asn Ser Ser 1 ace cca gee tgg ggt eee ggg cca eeg eet get eeg ggg gge age gge Thr Pro Ala Trp Gly Pro Gly Pro Pro Pro Ala Pro Gly Gly Ser Gly tgg gtg gct gcc gcg ctg tgc gtg gtc atc gtg ctg aca gca gcc gcc Trp Val Ala Ala Ala Leu Cys Val Val Ile Val Leu Thr Ala Ala Ala 30 35 aat tog otg otg ato gtg otc att tgo acg cag occ gcc gtg ogc aac 615 Asn Ser Leu Leu Ile Val Leu Ile Cys Thr Gln Pro Ala Val Arg Asn 45 50

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	_						gcc Ala									711
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_	_	_	_	_			ctc Leu 115			_			-	_	-	807
_		_				_	ccg Pro									855
_	_	_	-				atc Ile									903
	_						ttg Leu									951
							cag Gln									999
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	_				_		atc Ile		_	_	_	_	_	_		1095
							acg Thr									1143
	_	_					cca Pro	_			_			_	_	1191
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. 270 275 280

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tgc atc tcc cca ggc ctc ttc gat gtc ctc aca tgg ctg ggg tac tgt Cys Ile Ser Pro Gly Leu Phe Asp Val Leu Thr Trp Leu Gly Tyr Cys 300 305 310	1565											
aat agc acc atg aac cct atc atc tac ccg ctc ttt atg cgg gac ttc Asn Ser Thr Met Asn Pro Ile Ile Tyr Pro Leu Phe Met Arg Asp Phe 315 320 325	1613											
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ccc acc agg gcc acc act gtg gtc aac ttc ttt gtc aca gac tct gtg Pro Thr Arg Ala Thr Thr Val Val Asn Phe Phe Val Thr Asp Ser Val 410 415 420	1901											
gag cct gag ata cgg ccg cat cca ctc agt tcc ccc gtg aac Glu Pro Glu Ile Arg Pro His Pro Leu Ser Ser Pro Val Asn 425 430 435	1943											
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<212> PRT

. <213> Rat

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_	_	_								atc Ile					506
										ctg Leu 135					554
										agc Ser					602
										gag Glu					650
		_			_	_	_	_	_	gcc Ala	_			_	698
			_							ccc Pro					746
			_			_				cgc Arg 215					794
	_									cag Gln					842
_	_		_	_	_					gag Glu	_	 _	~	-	890
_		_		_	_	_				ctg Leu					938
										acc Thr					986
	_									tgc Cys 295					1034
										aac Asn					1082

atc atc tac cca ctc ttc atg ctg gac ttc aag cgg gcg ctg ggc agg

atc atc tac cca ctc ttc atg ctg gac ttc aag cgg gcg ctg ggc agg 1130

Ile Ile Tyr Pro Leu Phe Met Leu Asp Phe Lys Arg Ala Leu Gly Arg
320 325 330

ttc ctg cca tgt cca cgc tgt ccc cgg gag ccc agg cca gcc tgg cct

Phe Leu Pro Cys Pro Arg Cys Pro Arg Glu Pro Arg Pro Ala Trp Pro

335

340

345

cgc cat cac tgc gca cct ctc aca gcg gcc ccc ggc ccg gcc tta gcc 1226
Arg His His Cys Ala Pro Leu Thr Ala Ala Pro Gly Pro Ala Leu Ala
350 355 360

tac agc agg tgc tgc cgc tgc ccc tgc cgc cgg act cag att cgg act
Tyr Ser Arg Cys Cys Arg Cys Pro Cys Arg Arg Thr Gln Ile Arg Thr
365 370 375 380

cag acg cag gct cag gcg gct cct cgg gcg tgc ggc tca cgg ccc agc 1322
Gln Thr Gln Ala Gln Ala Ala Pro Arg Ala Cys Gly Ser Arg Pro Ser
385 390 395

tgc tgc ttc ctg gcg agg cca ccc agg acc ccc cgc tgc cca cca ggg 1370 Cys Cys Phe Leu Ala Arg Pro Pro Arg Thr Pro Arg Cys Pro Pro Gly 400 405 410

ccg ctg ccg ccg tca att tct tca aca tcg sac ccc gcg gag ccc gag 1418
Pro Leu Pro Pro Ser Ile Ser Ser Thr Ser Xaa Pro Ala Glu Pro Glu
415 420 425

ctg cgg ccg cat cca ctt ggc atc ccc acg aac tga cccggcttgg 1464 Leu Arg Pro His Pro Leu Gly Ile Pro Thr Asn *
430 435

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Val 65		Leu	Phe	Thr	Ser 70	Asp	Leu	Met	Val	Gly 75	Leu	Val	Val	Met	Pro 80
Pro	Ala	Met	Leu	Asn 85	Ala	Leu	Tyr	Gly	Arg 90	Trp	Val	Leu	Ala	Arg 95	Gly
Leu	Cys	Leu	Leu 100	Trp	Thr	Ala	Phe	Asp 105	Val	Met	Cys	Cys	Ser 110	Ala	Ser
Ile	Leu	Asn 115	Leu	Cys	Leu	Ile	Ser 120	Leu	Asp	Arg	Tyr	Leu 125	Leu	Ile	Leu
	130		Arg			135					140				
145			Gly	_	150					155					160
			Gly	165					170					175	
-		_	Arg 180					185					190		
_		195	Phe				200	_				205			
	210		Leu			215					220				
225		_	Met		230					235					240
			Ala	245					250					255	
			Arg 260					265					270		
	_	275	Phe Val				280					285			
	290		Gly			295					300				
305	_		Leu		310					315					320
			Pro	325		_			330					335	
			340 Thr					345					350		
		355	Pro				360					365			
	370		Pro			375					380				
385			Pro		390					395					400
			Ser	405			_	_	410		_			415	
			420 Ile				110	425	Ų.Lu	110	Jiu	Lou	430		
110	Leu	435	110	110	****	11011									